

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/29 08:24:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779335.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR1779335 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779335_1.fastq.gz SRR1779335_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Mar 29 08:24:50 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779335.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	148,612,570
Mapped reads	143,602,424 / 96.63%
Unmapped reads	5,010,146 / 3.37%
Mapped paired reads	143,602,424 / 96.63%
Mapped reads, first in pair	72,519,248 / 48.8%
Mapped reads, second in pair	71,083,176 / 47.83%
Mapped reads, both in pair	141,373,058 / 95.13%
Mapped reads, singletons	2,229,366 / 1.5%
Secondary alignments	0
Supplementary alignments	620,196 / 0.42%
Read min/max/mean length	30 / 100 / 100.06
Duplicated reads (estimated)	9,465,252 / 6.37%
Duplication rate	6.25%
Clipped reads	8,155,218 / 5.49%

2.2. ACGT Content

Number/percentage of A's	4,186,890,235 / 29.42%
Number/percentage of C's	2,912,730,114 / 20.47%
Number/percentage of T's	4,160,553,850 / 29.24%
Number/percentage of G's	2,968,738,697 / 20.86%
Number/percentage of N's	668,751 / 0%

GC Percentage	41.33%
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2.3. Coverage

Mean	4.5977
Standard Deviation	7.6339

2.4. Mapping Quality

Mean Mapping Quality	54
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2.5. Insert size

Mean	48,407.38
Standard Deviation	2,188,733.34
P25/Median/P75	165 / 220 / 298

2.6. Mismatches and indels

General error rate	0.41%
Mismatches	56,216,756
Insertions	1,513,611
Mapped reads with at least one insertion	1.04%
Deletions	1,508,963
Mapped reads with at least one deletion	1.03%
Homopolymer indels	47.95%

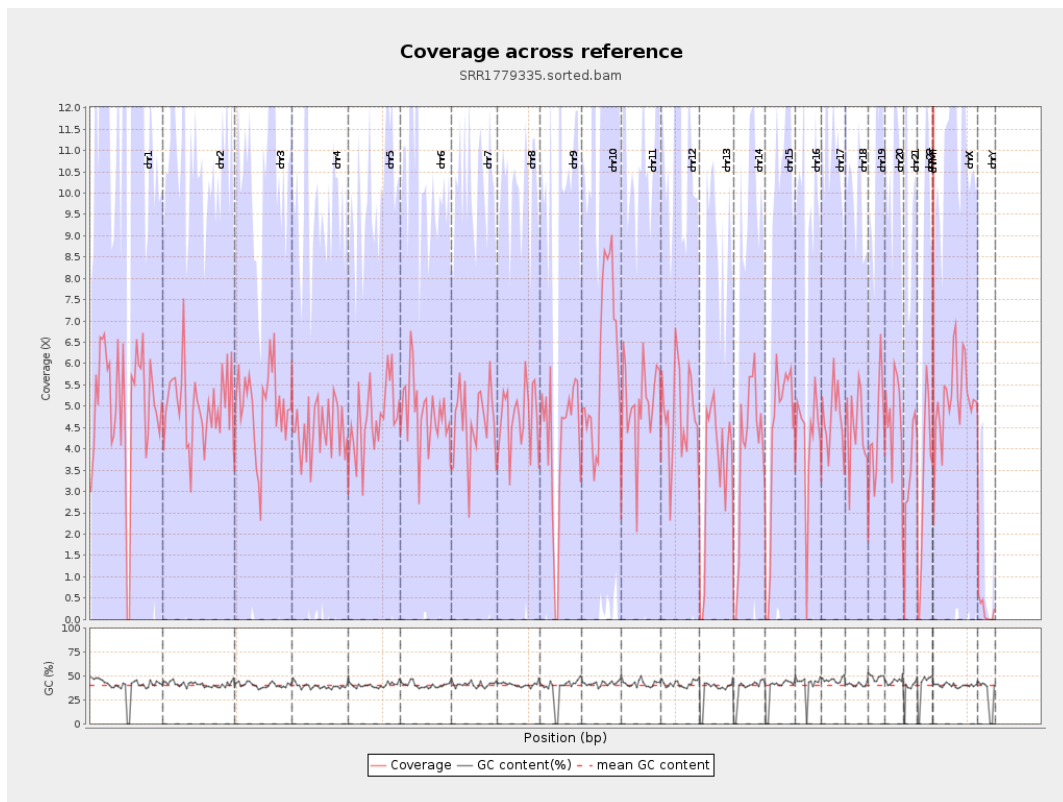
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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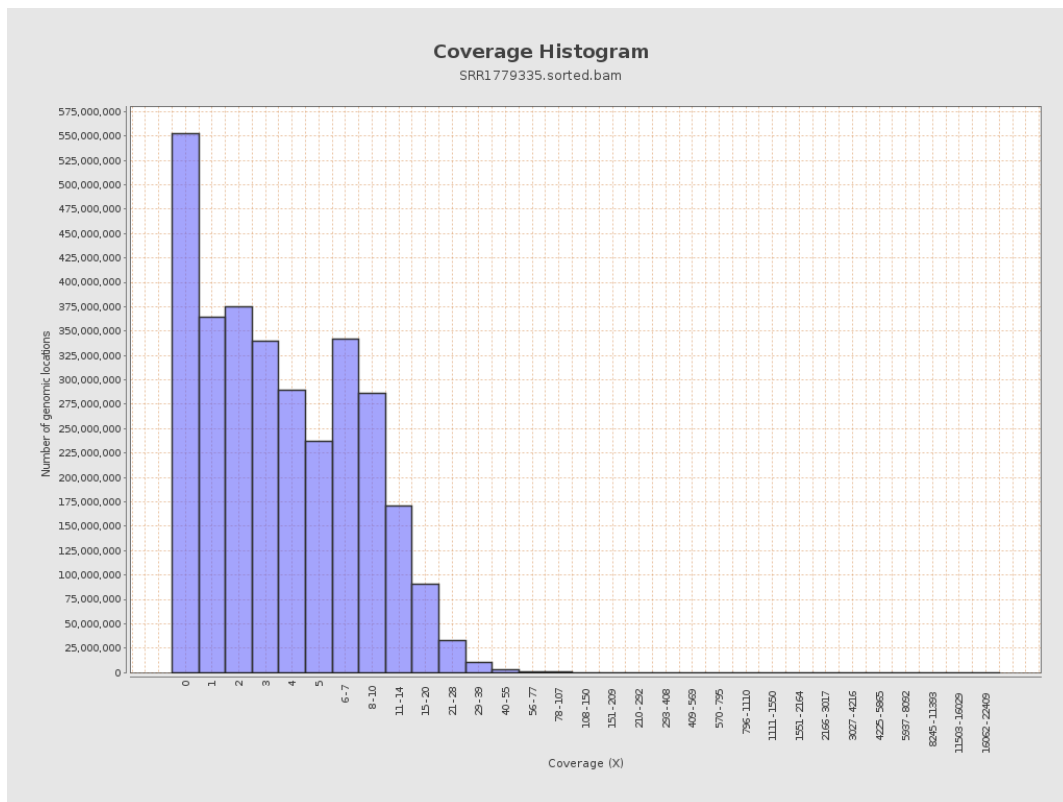
		bases	coverage	deviation
chr1	249250621	1244854494	4.9944	7.9476
chr2	243199373	1212460280	4.9855	18.2952
chr3	198022430	983922226	4.9687	5.0541
chr4	191154276	850508873	4.4493	5.6143
chr5	180915260	853810735	4.7194	4.8571
chr6	171115067	827436726	4.8356	5.5032
chr7	159138663	733616058	4.6099	5.3299
chr8	146364022	693959451	4.7413	4.9336
chr9	141213431	585698957	4.1476	5.7836
chr10	135534747	822747870	6.0704	8.5171
chr11	135006516	681815290	5.0502	5.4321
chr12	133851895	656010575	4.901	5.8075
chr13	115169878	406582232	3.5303	4.2741
chr14	107349540	423748521	3.9474	4.8174
chr15	102531392	432649445	4.2197	5.1488
chr16	90354753	377279482	4.1755	5.209
chr17	81195210	389456291	4.7965	6.0513
chr18	78077248	350137467	4.4845	5.549
chr19	59128983	255010630	4.3128	6.6335
chr20	63025520	298542292	4.7368	5.4679
chr21	48129895	164895586	3.4261	7.8459
chr22	51304566	168432330	3.283	4.9183
chrMT	16571	3776672	227.9085	70.1714
chrX	155270560	803697517	5.1761	5.3735

chrY	59373566	11869697	0.1999	2.2739
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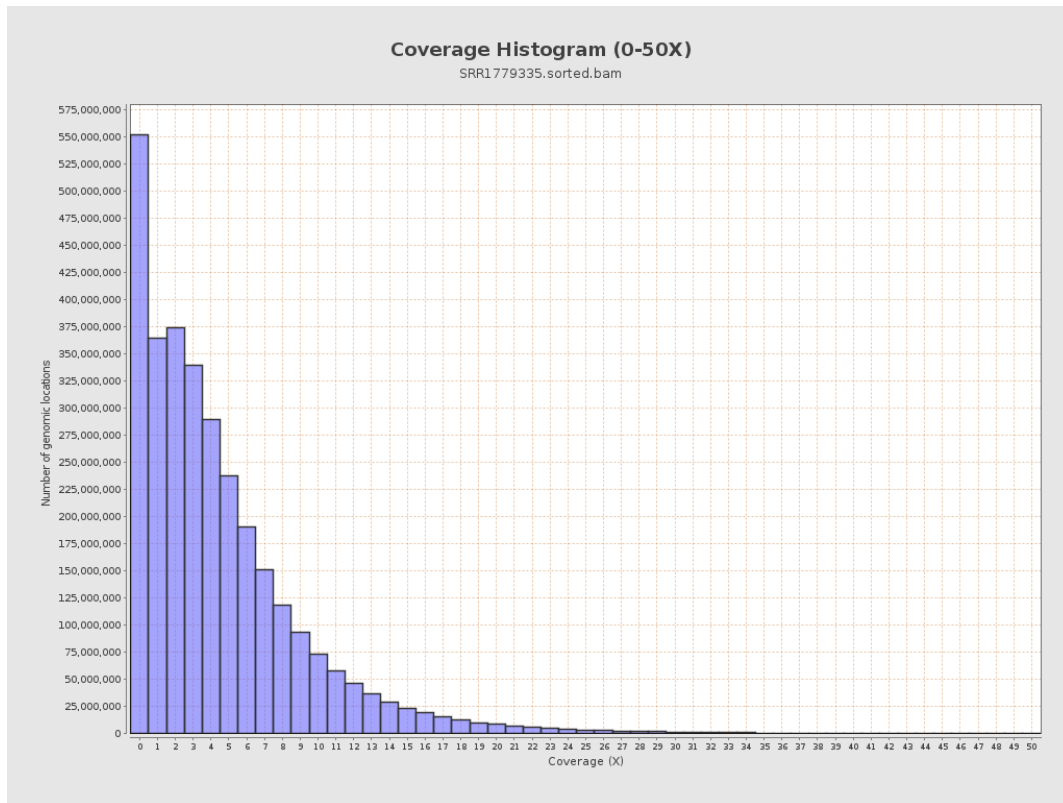
3. Results : Coverage across reference



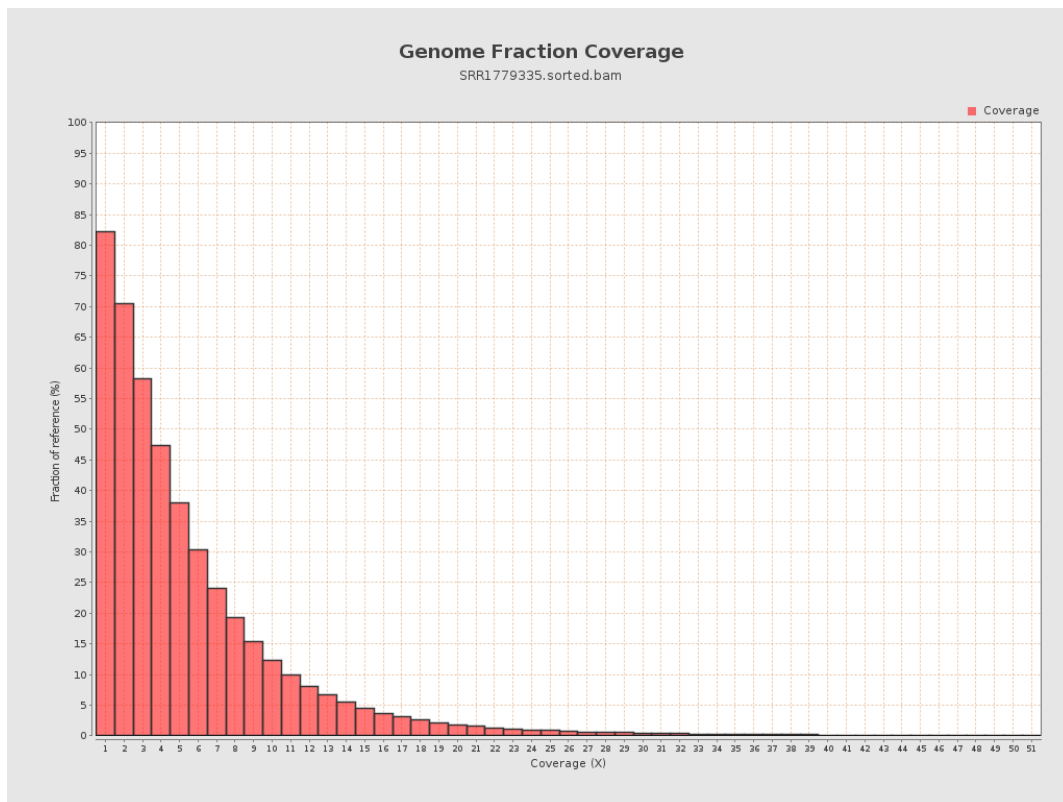
4. Results : Coverage Histogram



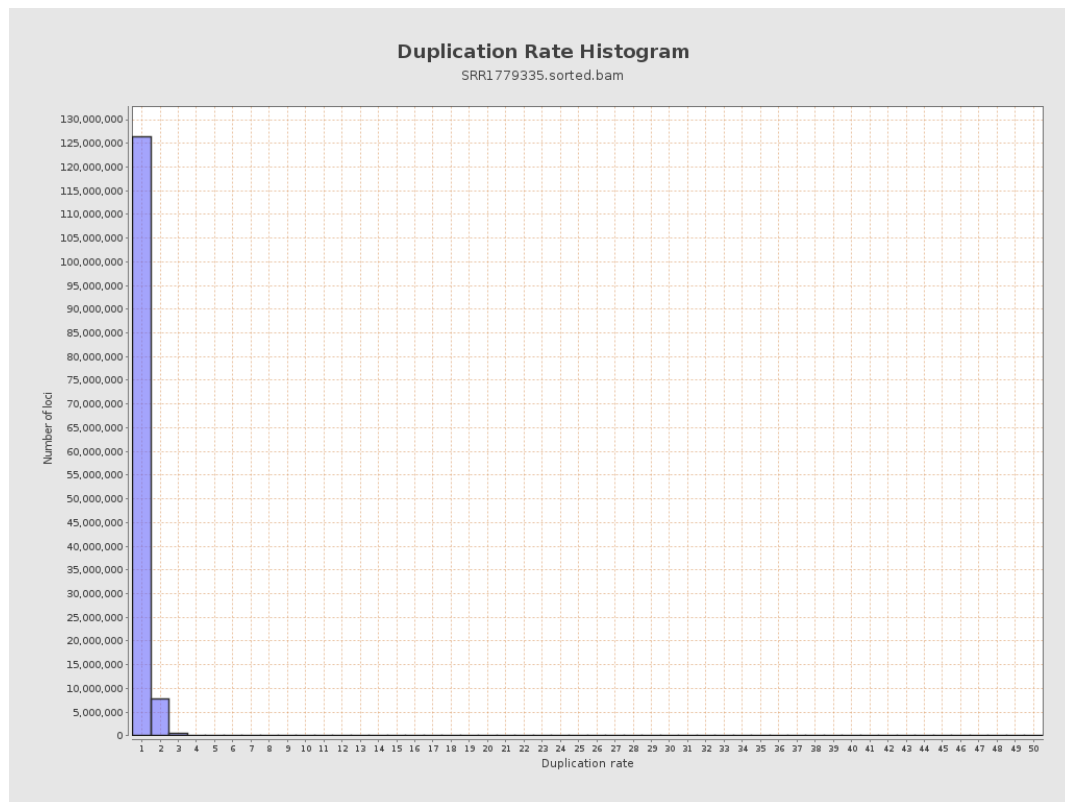
5. Results : Coverage Histogram (0-50X)



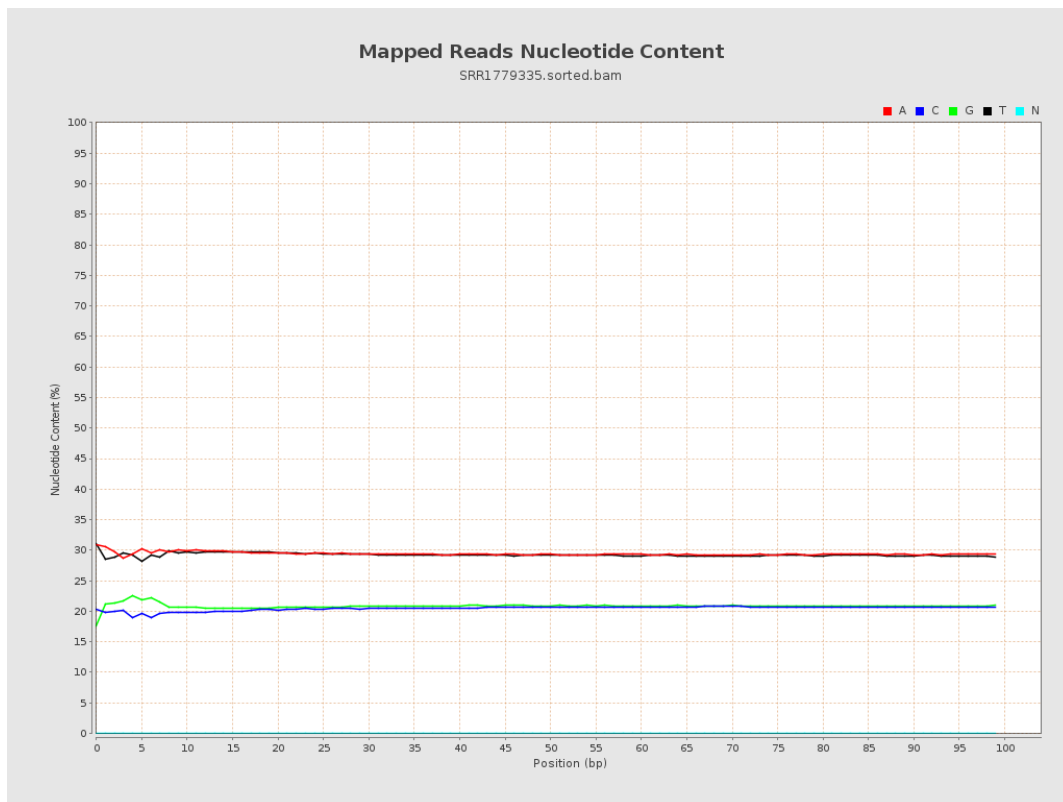
6. Results : Genome Fraction Coverage



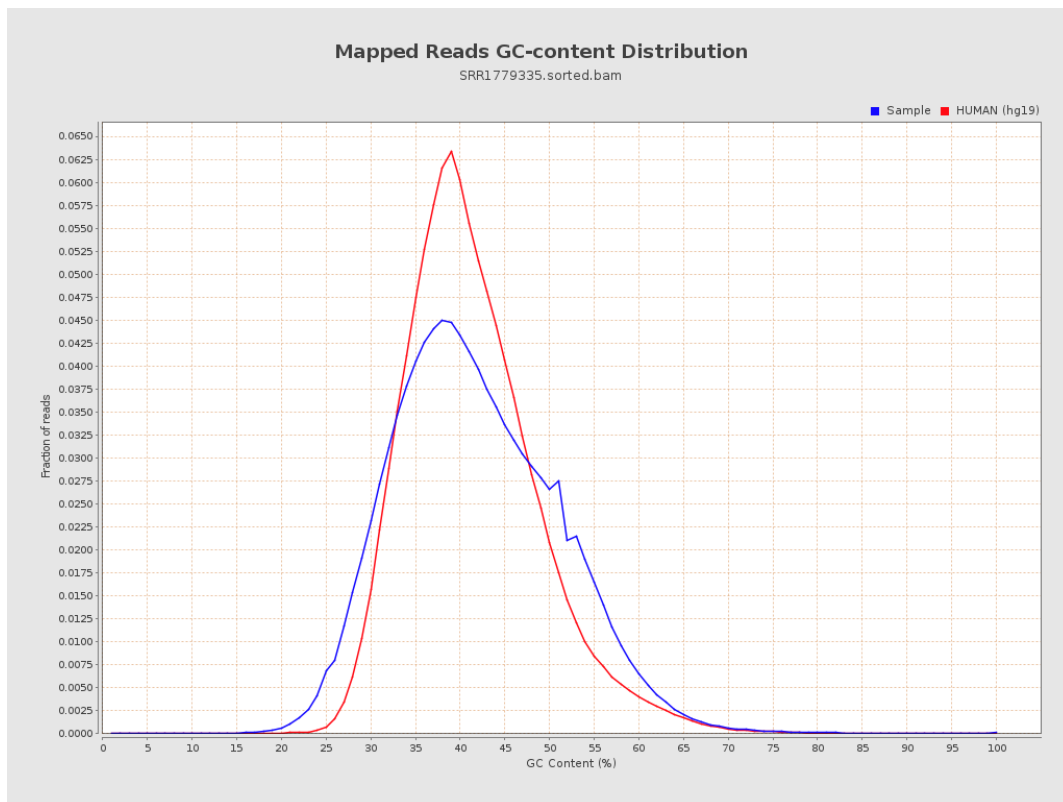
7. Results : Duplication Rate Histogram



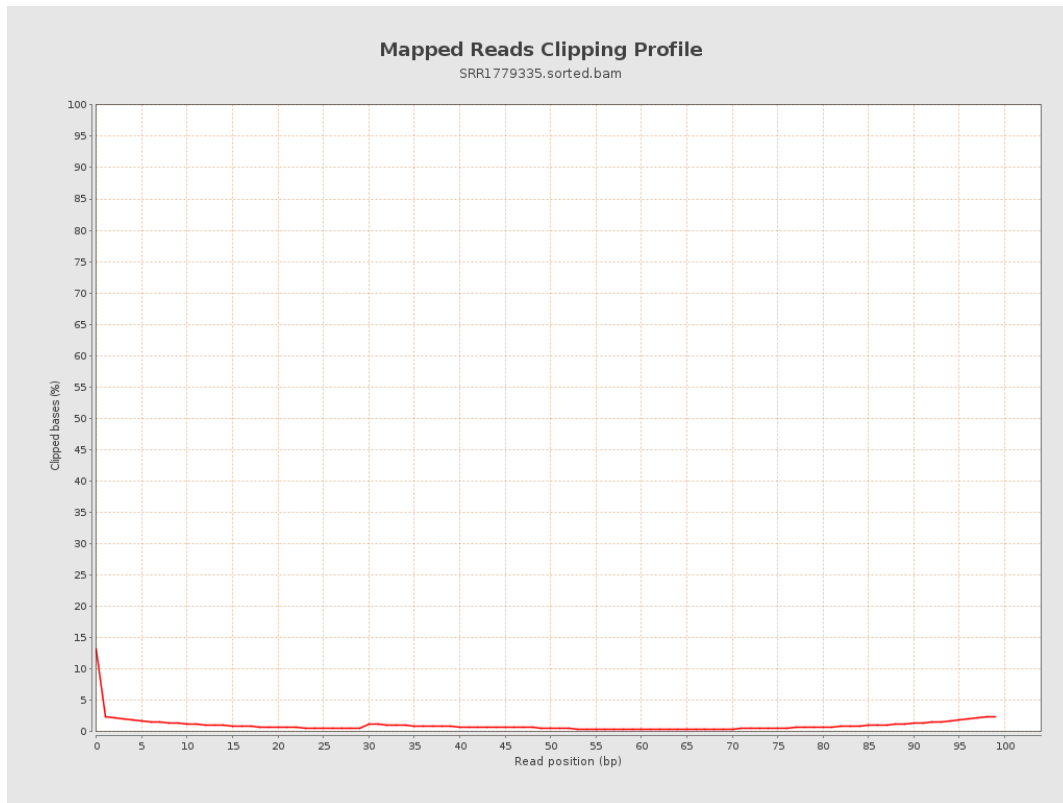
8. Results : Mapped Reads Nucleotide Content



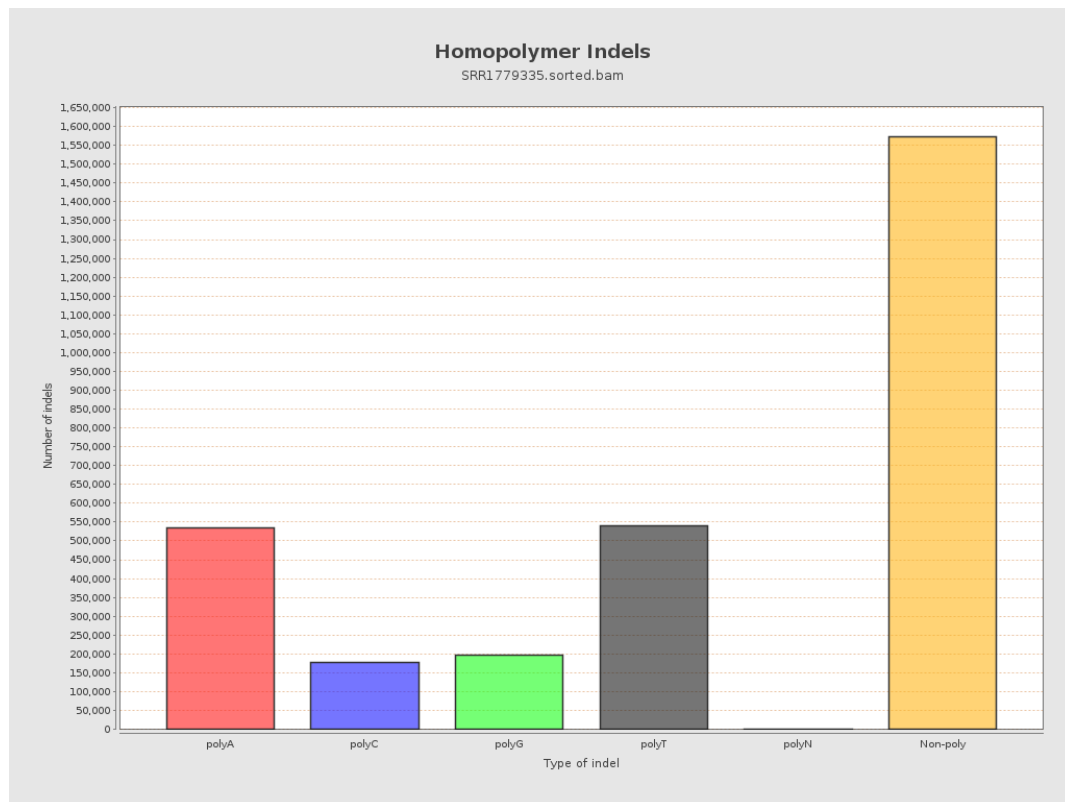
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



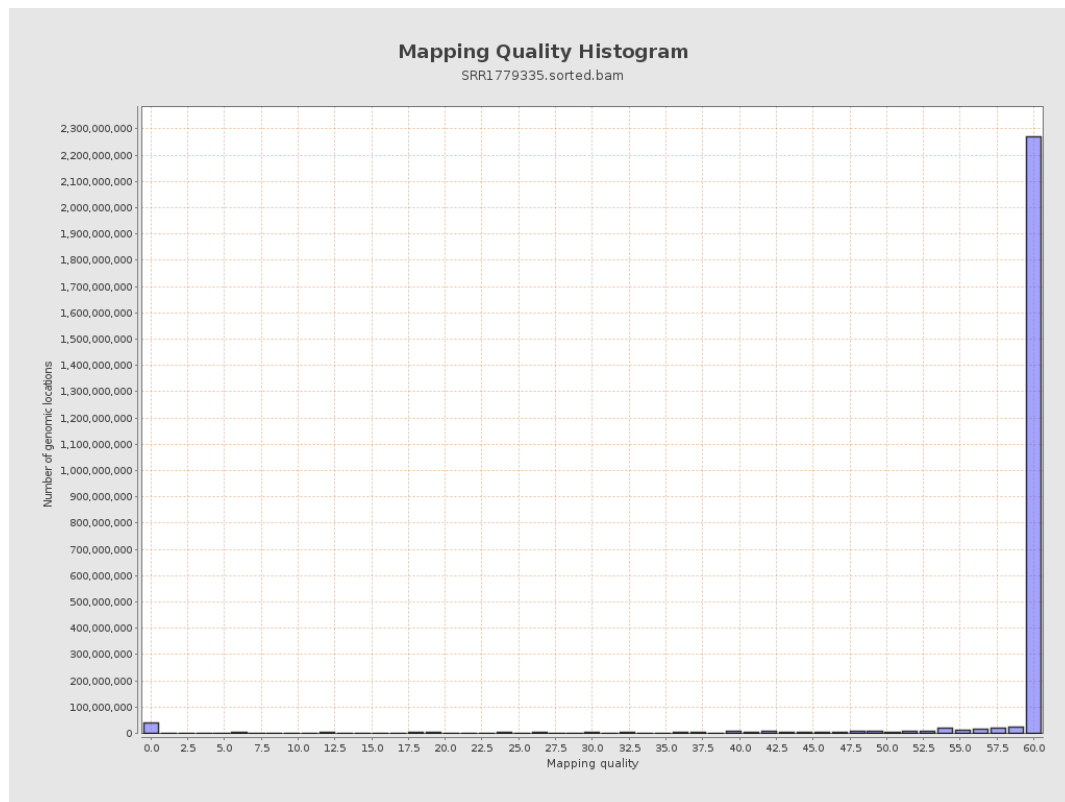
11. Results : Homopolymer Indels



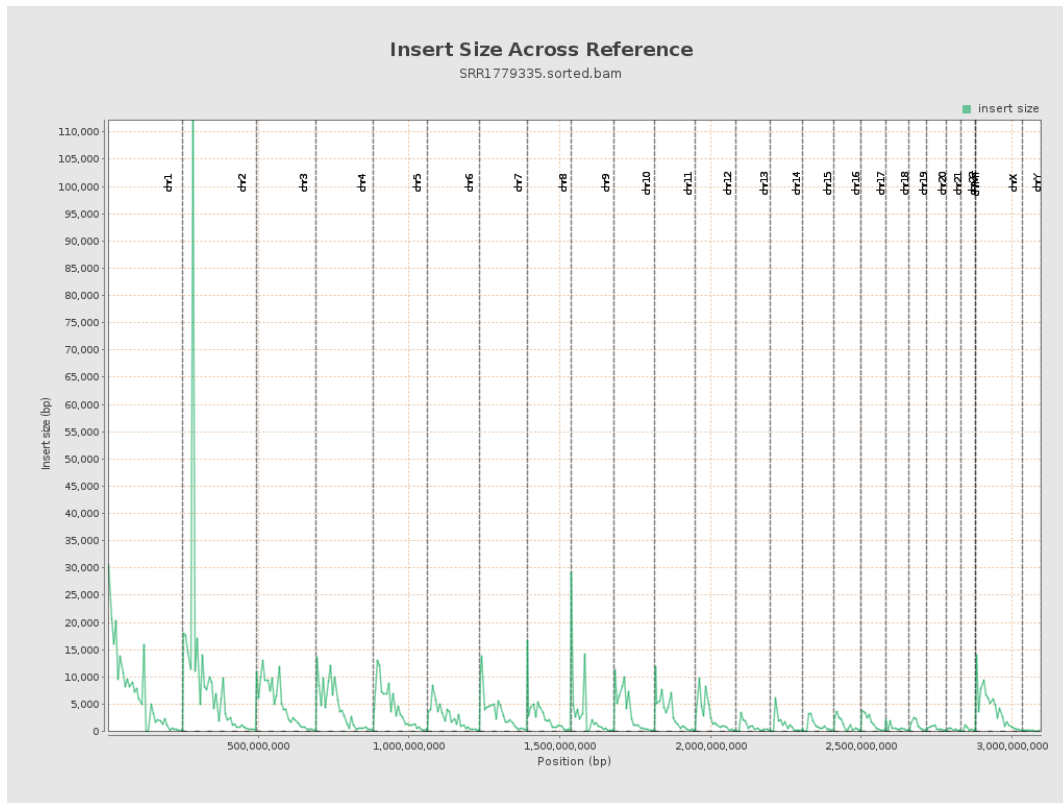
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

